Homologs of the *S. pombe* UVDE protein have been identified by BLAST searching of sequence database (Genbank, TIGR) using the UVDE amino acid sequence: *N. crassa* (Genbank Accession No. BAA 74539), *B. subtilis* (Genbank Accession No. 249782), human (Genbank Accession No. AF 114784.1, methyl-CpG binding endonuclease) and a *Deinococcus radiodurans* sequence located from the TIGR database. The amino acid sequences of these proteins are given in SEQ ID NO:36 (*N. crassa*), SEQ ID NO:37 (*B. subtilis*), SEQ ID NO:38 (*Homo sapiens*) and SEQ ID NO:39 (*D. radiodurans*). The *D. radiodurans* coding sequence can be generated using the genetic code and codon choice according to the recombinant host in which the protein is to be expressed, or the natural coding sequence can be found on the TIGR database, *D. radiodurans* genomic sequence in the region between bp 54823 and 60981. Additional homologs of the *S. pombe* UVDE include the UV damage enzyme of *Bacillus anthracis*; *Halobacterium* sp., disclosed in Genbank Accession No. AAC 82899; *Methanococcus jannaschii,* disclosed in Genbank Accession No. 057597; and *Thermotoga maritima*, disclosed in Genbank Accession No. AE001740. These homologs were identified using Blast or FastA on the NCBI or TIGR websites. A Uve1p consensus sequence has been derived using the vector NTI AlignX program. This consensus sequence spans amino acids 308-465 of the C-terminal region of the *S. pombe* Uve1p. This region shows significant sequence similarity to portions of the *B. subtilis* and *N. crassa* Uve1p equivalents.

B1

In the Claims:

16-20. Canceled without prejudice herein.

21. (New) A method for cleavage of a double-stranded DNA molecule characterized by a distorted structure, wherein said distorted structure results from ultraviolet radiation damage, a photoproduct, an abasic site, mismatched nucleotide pairing, a platinum diadduct, an intercalated molecule, an insertion deletion loop of five or fewer nucleotides or alkylation of a nucleotide or a uracil residue resulting from deamination of a cytosine residue, said method comprising the step of contacting a DNA molecule characterized by a distorted structure with a broadly specific DNA damage endonuclease selected from the

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